Baskar, P.
10/712654

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FILE LAST UPDATED: 18 Apr 2006 (20060418/ED)

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-key terms

L1 63345 SEA FILE=CAPLUS ABB=ON PLU=ON (OLIGONUCLEOTIDE OR OLIGO NUCLEOTIDE OR PROBE) AND (HYBRIDIS? OR HYBRIDIZ?)
L2 9 SEA FILE=CAPLUS ABB=ON PLU=ON L1 AND (PAGA OR PAG A OR CAPB OR CAP B)

L2 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 20 Sep 2005
ACCESSION NUMBER: 2005:1012869 CAPLUS
DOCUMENT NUMBER: 144:247943
TITLE: Development of a multipathogen **oligonucleotide** microarray for detection of Bacillus anthracis
AUTHOR(S): Burton, Jane E.; Oshota, O. James; North, Emma; Hudson, Michael J.; Polyanskaya, Natasha; Brehm, John; Lloyd, Graham; Silman, Nigel J.
CORPORATE SOURCE: Centre for Emergency Preparedness and Response, Health Protection Agency, Porton Down, Salisbury, Wiltshire, SP4 0JG, UK
SOURCE: Molecular and Cellular Probes (2005), 19(5), 349-357
CODEN: MCPRE6; ISSN: 0890-8508
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB An **oligonucleotide** microarray system has been specifically designed to detect and differentiate Bacillus anthracis from other bacterial species present in clin. samples. The pilot-scale microarray initially incorporated **probes** to detect six common species of bacteria, which were fully evaluated. The microarray comprised long **oligonucleotides** (50-70-mer) designed to **hybridize** with the variable regions of the 16S rRNA genes. **Probes** which **hybridized** to virulence genes were also incorporated; for B. anthracis, these initially included the pag, lef, cap and vrrA (for partial genotyping) genes. **Hybridization** conditions were initially optimized to be run

using 5+SSC, 0.1% SDS, 50 °C for 16 h. The detection limits of the microarray were determined under these conditions by titration of chromosomal DNA and unlabeled amplicons followed by **hybridization** to determine the levels of sensitivity that could be obtained with the microarray. Two different amplification methodologies were also compared-specific-primer based PCR and random PCR (with the labeling stage incorporated). Higher sensitivity was obtained using specific PCR primers, however, since one of the desired outcomes of a microarray-based detection system was the high discrimination that it offered, random amplification and labeling was used as the amplification method of choice. The length of **hybridization** was investigated using a time-course, and 1-2 h was found to give optimal and higher signals than 16 h incubation. These results indicate that microarray technol. can be employed in a diagnostic environment and moreover, results may be obtained in a similar time-scale to a standard PCR reaction, but with the advantage that no a priori knowledge of the infectious agent is required for detection.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 29 Jun 2005
ACCESSION NUMBER: 2005:559843 CAPLUS
DOCUMENT NUMBER: 143:167605
TITLE: Preparation of gene chip for diagnosing Anthrax and its application
INVENTOR(S): Wang, Shengqi; Chen, Suhong; Zhang, Minli
PATENT ASSIGNEE(S): Radioactive Medicine Inst., Academy of Military Medicine, PLA, Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, No pp. given
CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 1537953	A	20041020	CN 2003-121884	20030417
PRIORITY APPLN. INFO.:			CN 2003-121884	20030417

AB A process for preparing the gene chip for diagnosing anthrax bacillus is disclosed. Said gene chip can be used in conjunction with PCR technique to detect the plasmids PXO1 and PXO2 and the chromosome of Anthrax and to analyze them at same time. Its advantage is high specificity and sensitivity.

L2 ANSWER 3 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 20 Aug 2004
ACCESSION NUMBER: 2004:681670 CAPLUS
DOCUMENT NUMBER: 141:201314
TITLE: Assay and compositions for detection of Bacillus anthracis nucleic acid
INVENTOR(S): Norman, Sylvia A.; Bungo, Jennifer J.; Hogan, James J.; Weisburg, William G.
PATENT ASSIGNEE(S): Gen-Probe Incorporated, USA

SOURCE: PCT Int. Appl., 61 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004070001	A2	20040819	WO 2003-US36240	20031112
WO 2004070001	A3	20051201		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2506151	AA	20040819	CA 2003-2506151	20031112
EP 1572977	A2	20050914	EP 2003-815297	20031112
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				

PRIORITY APPLN. INFO.:			
US 2002-426552P	P	20021115
US 2003-471082P	P	20030516
WO 2003-US36240	W	20031112

AB The invention includes nucleic acid sequences and methods of detection of Bacillus anthracis that use **oligonucleotide probes** specific for genetic material contained in the pXO1 and pX02 plasmids in nucleic acid **hybridization** reactions. Embodiments of the method may include addnl. **probes** specific for other gene sequences to distinguish B. anthracis from other bacterial species present in a sample or to provide an indication that the assay was performed properly even when no Bacillus sequence is detected. The invention include **oligonucleotides** that **hybridize** to **capB** and **pagA** gene sequence.

L2 ANSWER 4 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 13 Jul 2004
ACCESSION NUMBER: 2004:557862 CAPLUS
DOCUMENT NUMBER: 141:375185
TITLE: Identification of Bacillus anthracis by multiprobe microarray **hybridization**
AUTHOR(S): Volokhov, Dmitriy; Pomerantsev, Andrei; Kivovich, Violetta; Rasooly, Avraham; Chizhikov, Vladimir
CORPORATE SOURCE: Center for Biologics Evaluation and Research, Food and Drug Administration, Kensington, MD, 20895, USA
SOURCE: Diagnostic Microbiology and Infectious Disease (2004), 49(3), 163-171
CODEN: DMIDDZ; ISSN: 0732-8893
PUBLISHER: Elsevier Science Inc.

DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have developed a rapid assay based on microarray anal. of amplified genetic markers for reliable identification of Bacillus anthracis and its discrimination from other closely related bacterial species of the Bacillus cereus group. By combining polymerase chain reaction (PCR) amplification of six B. anthracis-specific genes (plasmid-associated genes encoding virulence factors (cyaA, **pagA**, lef, and capA, **capB**, capC) and one chromosomal marker BA-5449) with anal. of amplicons by microarray **hybridization**, we were able to unambiguously identify and discriminate B. anthracis among other closely related species. Bacillus identification relied on **hybridization** with multiple individual microarray **oligonucleotide probes** (oligoprobes) specific to each target B. anthracis gene. Evaluation of the assay was conducted using several B. anthracis strains (with or without pXO1 and pXO2 plasmids) as well as over 50 other species phylogenetically related to B. anthracis, including B. cereus, B. thuringiensis, B. mycoides, and B. subtilis. The developed microarray anal. of amplified genetic markers protocol provides an efficient method for (i) unambiguous identification and discrimination of B. anthracis from other Bacillus species and (ii) distinguishing between plasmid-containing and plasmid-free Bacillus anthracis strains.
REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 08 Aug 2003
ACCESSION NUMBER: 2003:606704 CAPLUS
DOCUMENT NUMBER: 139:271584
TITLE: DNA **Hybridization** and Discrimination of Single-Nucleotide Mismatches Using Chip-Based Microbead Arrays
AUTHOR(S): Ali, Mehnaaz F.; Kirby, Romy; Goodey, Adrian P.; Rodriguez, Marc D.; Ellington, Andrew D.; Neikirk, Dean P.; McDevitt, John T.
CORPORATE SOURCE: Department of Chemistry & Biochemistry, Department of Electrical Computer Engineering, Center for Nano- and Molecular Science and Technology, Texas Materials Institute, Austin, TX, 78712, USA
SOURCE: Analytical Chemistry (2003), 75(18), 4732-4739
CODEN: ANCHAM; ISSN: 0003-2700
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The development of a chip-based sensor array composed of individually addressable agarose microbeads has been demonstrated for the rapid detection of DNA **oligonucleotides**. Here, a "plug and play" approach allows for the simple incorporation of various biotinylated DNA capture **probes** into the bead-microreactors, which are derivatized in each case with avidin docking sites. The DNA capture **probe** containing microbeads are selectively arranged in micromachined cavities localized on silicon wafers. The microcavities possess trans-wafer openings, which allow for both fluid flow through the microreactors/anal. chambers and optical access to the chemical sensitive microbeads. Collectively, these features allow the identification and quantitation of target DNA analytes to occur in near real time using fluorescence changes that accompany binding of

the target sample. The unique three-dimensional microenvironment within the agarose bead and the microfluidics capabilities of the chip structure afford a fully integrated package that fosters rapid analyses of solns. containing complex mixts. of DNA oligomers. These analyses can be completed at room temperature through the use of appropriate **hybridization** buffers. For applications requiring anal. of ≤102 different DNA sequences, the **hybridization** times and point mutation selectivity factors exhibited by this bead array method exceed in many respects the operational characteristics of the commonly utilized planar DNA chip technologies. The power and utility of this microbead array DNA detection methodol. is demonstrated here for the anal. of fluids containing a variety of similar 18-base **oligonucleotides**. **Hybridization** times on the order of minutes with point mutation selectivity factors greater than 10,000 and limit of detection values of .apprx.10-13 M are obtained readily with this microbead array system.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 25 Apr 2003
ACCESSION NUMBER: 2003:317507 CAPLUS
DOCUMENT NUMBER: 138:315823
TITLE: Detection of Bacillus anthracis by using real-time PCR
INVENTOR(S): Bell, Constance A.; Uhl, James R.; Cockerill, Franklin R.
PATENT ASSIGNEE(S): Roche Diagnostics G.m.b.H., Germany; Mayo Foundation for Medical Education and Research
SOURCE: Eur. Pat. Appl., 31 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
EP 1304387	A1	20030423	EP 2002-22398		20021010
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK					
US 2003082563	A1	20030501	US 2002-68238		20020205
PRIORITY APPLN. INFO.:			US 2001-329826P	P	20011015
			US 2002-68238	A	20020205

AB The invention provides methods to detect Bacillus anthracis in biol. or non-biol. samples using real-time PCR. Primers and **probes** for the detection of Bacillus anthracis are provided by the invention. Articles of manufacture containing such primers and **probes** as well as kits containing such primers and **probes** for detecting Bacillus anthracis are further provided by the invention. Using specific primers and **probes**, the methods include amplifying and monitoring the development of specific amplification products using fluorescence resonance energy transfer.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 25 Sep 1998
ACCESSION NUMBER: 1998:607911 CAPLUS
DOCUMENT NUMBER: 130:11218
TITLE: Identification of PhoP-PhoQ activated genes within a duplicated region of the Salmonella typhimurium chromosome
AUTHOR(S): Gunn, John S.; Belden, William J.; Miller, Samuel I.
CORPORATE SOURCE: Departments of Medicine and Microbiology, University of Washington, Seattle, WA, 98195, USA
SOURCE: Microbial Pathogenesis (1998), 25(2), 77-90
CODEN: MIPAEV; ISSN: 0882-4010
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Salmonellae virulence requires the PhoP-PhoQ two-component regulatory system. PhoP-PhoQ activate the transcription of genes following phagocytosis by macrophages which are necessary for survival within the phagosome environment. Thirteen previously undefined PhoP-activated gene fusions generated by MudJ and TnphoA (**pag A**, and E-P, resp.) were cloned and sequenced. Most pag products show no similarity to proteins in the database, while others are predicted to encode: a UDP-glucose dehydrogenase (**pagA**); a protein with similarity to the product of an E. coli aluminum-induced gene (pagH); a protein encoded within a Salmonella-unique region adjacent to the sinR gene (pagN); a protein similar to a product of the Yersinia virulence plasmid (pagO); and a protein with similarity to CrcA which is necessary for resistance of E. coli to camphor (pagP). Of the pag characterized, only pagK, M and O were closely linked, pagJ and pagK were shown to be unlinked but nearly identical in DNA sequence, as each was located within a 1.6 kb DNA duplication. The translations of sequences surrounding pagJ and pagK show similarity to proteins from extrachromosomal elements as well as those involved in DNA transposition and rearrangement, suggesting that this region may have been or is a mobile element. The transcriptional start sites of pagK, M, and J were determined; however, comparison to other known pag gene promoters failed to reveal a consensus sequence for PhoP-regulated activation. DNA sequences **hybridizing** to a Salmonella typhimurium pagK specific **probe** were found in S. enteritidis but absent in other Salmonella serotypes and Enterobacteriaceae tested, suggesting that these genes are specific for broad host range Salmonellae that cause diarrhea in humans. Cumulatively, these data further demonstrate: (1) that PhoP-PhoQ is a global regulator of the production of diverse envelope or secreted proteins; (2) that PhoP-PhoQ regulate the production of proteins of redundant function; and (3) the pag are often located in regions of horizontally acquired DNA that are absent in other Enterobacteriaceae. (c) 1998 Academic Press.
REFERENCE COUNT: 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 11 Nov 1994
ACCESSION NUMBER: 1995:178423 CAPLUS
DOCUMENT NUMBER: 122:48451
TITLE: Analysis by pulsed-field gel electrophoresis of

insertion mutations in the transferrin-binding system of Haemophilus influenzae type b
AUTHOR(S): Curran, R.; Hardie, K. R.; Towner, K. J.
CORPORATE SOURCE: Queen's Medical Centre, University Hospital, Nottingham, NG7 2UH, UK
SOURCE: Journal of Medical Microbiology (1994), 41(2), 120-6
CODEN: JMMIAV; ISSN: 0022-2615
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A mutagenesis system involving the insertion of a non-transposable antibiotic resistance gene cassette was used to generate stable mutations in the chromosome of Haemophilus influenzae type b strain Eagan. The mutations generated were shown by pulsed-field gel electrophoresis (PFGE) to have unique SmaI fingerprint patterns and to be located randomly on the chromosome. Of 700 insertion mutants screened, 29 had stable insertions resulting in constitutive expression of transferrin-binding proteins (TBPs). The high proportion of such mutants indicated that numerous regulatory loci could influence the expression of this phenotype. Five such regulatory mutations were analyzed in detail by PFGE and DNA **hybridization** and were shown to be located at five different chromosomal loci, although three of the five loci were located on the same 330-kb SmaI fragment of the wild-type strain Eagan chromosome. This fragment also contains several important virulence determinants, including the **capb** locus, and one of the five constitutive mutants had concomitantly lost the ability to synthesize a type-b capsule. No DNA homol. was demonstrated between H. influenzae chromosomal fragments separated by PFGE and DNA **probes** for the TBPs from Neisseria meningitidis, but the possibility of shared regulatory mechanisms controlling the expression of TBPs in these two species remains to be investigated.

L2 ANSWER 9 OF 9 CAPLUS COPYRIGHT 2006 ACS on STN
ED Entered STN: 23 Jul 1994
ACCESSION NUMBER: 1994:428011 CAPLUS
DOCUMENT NUMBER: 121:28011
TITLE: Identification of capsule-forming Bacillus anthracis spores with the PCR and a novel dual-**probe hybridization** format
AUTHOR(S): Reif, Timothy C.; Johns, Malcolm; Pillai, Suresh D.; Carl, Mitchell
CORPORATE SOURCE: Natl. Naval Med. Cent., Naval Med. Res. Inst., Bethesda, MD, 20889, USA
SOURCE: Applied and Environmental Microbiology (1994), 60(5), 1622-5
CODEN: AEMIDF; ISSN: 0099-2240
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Anthrax is a fatal infection of humans and livestock that is caused by the gram-pos. bacterium Bacillus anthracis. The virulent strains of B. anthracis are encapsulated and toxigenic. In this paper the authors describe the development of a PCR technique for identifying spores of B. anthracis. Two 20-mer **oligonucleotide** primers specific for the **capB** region of 60-MDa plasmid pXO2 were used for amplification. The amplification products were detected by using biotin- and fluorescein-labeled **probes** in a novel dual-**probe hybridization** format. Using the combination of PCR amplification and dual-**probe**

hybridization, the authors detected two copies of the bacterial genome. Because the PCR assay could detect a min. of 100 unprocessed spores per PCR mixts., the authors attempted to facilitate the release of DNA by comparing the effect of limited spore germination with the effect of mech. spore disruption prior to PCR amplification. The two methods were equally effective and allowed the authors to identify single spores of B. anthracis in PCR mixts.

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FILE 'JAPIO' ENTERED AT 17:11:40 ON 19 APR 2006
COPYRIGHT (C) 2006 Japanese Patent Office (JPO)- JAPIO

L3 24 S L2
L4 12 DUP REM L3 (12 DUPLICATES REMOVED)

L4 ANSWER 1 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2006-067458 [07] WPIDS
DOC. NO. CPI: C2006-024783
TITLE: New antibody that specifically binds to a cellular antigen that is detectably expressed by CD36+ fetal liver cells, but not by CD36+ adult peripheral blood cells, useful for detecting fetal cells in a biological fluid.
DERWENT CLASS: B04 D16
INVENTOR(S): ELIAS, S; SHARMA, A
PATENT ASSIGNEE(S): (UNII) UNIV ILLINOIS FOUND
COUNTRY COUNT: 111
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2005123779	A2	20051229	(200607)*	EN	57

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IS IT KE LS LT LU MC MW MZ NA NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KM KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NG NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SM SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2005123779	A2	WO 2005-US20884	20050613

PRIORITY APPLN. INFO: US 2004-618963P 20041015; US 2004-579693P 20040614

AN 2006-067458 [07] WPIDS

AB WO2005123779 A UPAB: 20060130

NOVELTY - An antibody that specifically binds to a cellular antigen that is detectably expressed by CD36+ fetal liver cells, but not detectably expressed by CD36+ adult peripheral blood cells, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) isolating fetal cells from a biological fluid;

(2) detecting fetal cells in a biological fluid;

(3) a diagnostic method where the fetal cells are genetically evaluated using FISH, PCR or real time PCR; and

(4) producing an antibody that specifically binds to cell surface antigens that are detectably expressed by CD36+ fetal liver cells, but not detectably expressed by CD36+ adult peripheral blood cells.

USE - The antibody is useful for detecting fetal cells in a biological fluid, including maternal peripheral blood (claimed).

Dwg.0/2

L4 ANSWER 2 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2005-460886 [47] WPIDS

DOC. NO. CPI: C2005-140330

TITLE: Fabricating an array of polymers e.g. **oligonucleotides**, comprises coating a substrate containing a protected reactive group with a film containing activatable deprotecting agent followed by activating at selected areas.

DERWENT CLASS: A89 B04 D16

INVENTOR(S): GOLDBERG, M J; KUIMELIS, R G; MCGALL, G H; PARKER, N; XU, G; PARKER, N A

PATENT ASSIGNEE(S): (AFFY-N) AFFYMETRIX INC

COUNTRY COUNT: 38

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1547678	A2	20050629	(200547)*	EN	16
R: AL AT BA BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK NL PL PT RO SE SI SK TR YU					
CA 2490675	A1	20050622	(200547)	EN	
US 2005164258	A1	20050728	(200550)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
EP 1547678	A2		EP 2004-258031	20041222
CA 2490675	A1		CA 2004-2490675	20041222
US 2005164258	A1	Provisional	US 2003-532220P	20031222
		Provisional	US 2004-577050P	20040603
			US 2004-21700	20041222

PRIORITY APPLN. INFO: US 2004-577050P 20040603; US
2003-532220P 20031222; US
2004-21700 20041222
AN 2005-460886 [47] WPIDS
AB EP 1547678 A UPAB: 20050725
NOVELTY - Fabricating an array of polymers by:
(a) coating a solid substrate containing a reactive group (R1) protected by a protective group with a film containing an activatable deprotecting agent (D1);
(b) activating (D1) in selected areas by selective application of an activator; and
(c) exposing (R1) to activated (D1) for removing the protecting group to obtain a monomer with an exposed reactive group.
DETAILED DESCRIPTION - Fabricating an array of polymers comprises:
(a) coating a solid substrate containing a reactive group (R1) protected by a protective group with a film containing an activatable deprotecting agent (D1);
(b) activating (D1) in selected areas by selective application of an activator to provide activated (D1); and
(c) exposing (R1) to activated (D1) for removing the protecting group to obtain a monomer with an exposed reactive group.
USE - For fabricating an array of polymers such as an array of nucleic acid, DNA-**oligonucleotides** or peptides (claimed) particularly useful for solid phase combinatorial synthesis of polymer arrays useful in e.g. gene therapy for detecting mutations and polymorphisms, for assaying gene expression monitoring, nucleic acid amplification and analysis. Also useful for screening compounds having activities, for detection of **hybridization**.
ADVANTAGE - The method provides array of polymers in high-yields with reduction or elimination of depurination as post-activation baking step is avoided. The step of exposing and the photoacids used, cause minimal or insubstantial damage to the polymers. The polymer arrays produced have desirable features in the order of 10 - 100 (preferably 1 - 10) micro m or 100 - 1000 nm. The protective groups are cleaved using activatable deprotecting reagents to achieve a high sensitive, high resolution combinatorial synthesis of pattern arrays of diverse polymers.
Dwg.0/0

L4 ANSWER 3 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-604428 [58] WPIDS
DOC. NO. CPI: C2004-219027
TITLE: New **oligonucleotides** that **hybridize** specifically to a Bacillus anthracis sequence, useful for detecting cutaneous and respiratory Bacillus anthrax infections.
DERWENT CLASS: B04 D16
INVENTOR(S): BUNGO, J J; HOGAN, J J; NORMAN, S A; WEISBURG, W G
PATENT ASSIGNEE(S): (GENP-N) GEN-PROBE INC
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004070001	A2	20040819	(200458)*	EN	61

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT

KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE
DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE
KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO
NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ
UA UG US UZ VC VN YU ZA ZM ZW
AU 2003303307 A1 20040830 (200480)
EP 1572977 A2 20050914 (200560) EN
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LI LT LU
LV MC MK NL PT RO SE SI SK TR

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004070001	A2	WO 2003-US36240	20031112
AU 2003303307	A1	AU 2003-303307	20031112
EP 1572977	A2	EP 2003-815297	20031112
		WO 2003-US36240	20031112

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003303307	A1 Based on	WO 2004070001
EP 1572977	A2 Based on	WO 2004070001

PRIORITY APPLN. INFO: US 2003-471082P 20030516; US 2002-426552P 20021115

AN 2004-604428 [58] WPIDS

AB WO2004070001 A UPAB: 20040910

NOVELTY - An **oligonucleotide** of 20-40 nucleotides that specifically **hybridizes** to a sequence contained in a Bacillus anthracis target sequence consisting of any of 7 fully defined sequences of 50-560 base pairs (bp) (SEQ ID NO: 2-16 and 34), its complementary sequence, or RNA equivalent of any one of the target sequences, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) an **oligonucleotide** of 18-40 or 20-50 bases that **hybridizes** specifically to a 16S or 23S rRNA or DNA, respectively, encoding a 16S or 23S rRNA sequence of a Bacillus species contained in a target sequence consisting of a fully defined sequence of 95 or 80 base pairs (bp) (SEQ ID NO: 32), respectively, or its complementary sequence or RNA equivalent;

(2) detecting B. anthracis nucleic acid in a sample, comprising providing a sample containing B. anthracis nucleic acids, providing at least one **probe** that **hybridizes** specifically to a **pagA** target sequence contained in a pXO1 plasmid and at least one **probe** that **hybridizes** specifically to a **capB** target sequence contained in a pXO2 plasmid, **hybridizing** specifically at least one **probe** to the **pagA** or **capB** target sequence, or at least one **probe** to the **capB** or **pagA** target sequence, and detecting the presence of at least one **probe** **hybridized** to the **pagA** target sequence or to the **capB** target sequence to indicate the presence of B. anthracis in the sample; and

(3) a kit for practicing the method of (2), comprising at least one **probe** that **hybridizes** to a sequence contained

in the **pagA** target sequence consisting of SEQ ID NO: 21-24, or its complementary sequence or RNA equivalent, and at least one **probe** that **hybridizes** specifically to a sequence contained in the **capB** target sequence consisting of SEQ ID NO: 25 or 26, or its complementary sequence, or RNA equivalent of any one of these sequences.

USE - The methods and compositions of the present invention are useful for detecting the presence of Bacillus anthracis nucleic acid in a sample, in particular for detecting cutaneous and respiratory anthrax infections (claimed).

Dwg.0/0

L4 ANSWER 4 OF 12 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2004343006 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15246505
TITLE: Identification of Bacillus anthracis by multiprobe microarray **hybridization**.
AUTHOR: Volokhov Dmitriy; Pomerantsev Andrei; Kivovich Violetta; Rasooly Avraham; Chizhikov Vladimir
CORPORATE SOURCE: Center for Biologics Evaluation and Research, Food and Drug Administration, Kensington, MD 20895, USA.
SOURCE: Diagnostic microbiology and infectious disease, (2004 Jul) Vol. 49, No. 3, pp. 163-71.
Journal code: 8305899. ISSN: 0732-8893.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 20040713
Last Updated on STN: 20041006
Entered Medline: 20041005

AB We have developed a rapid assay based on microarray analysis of amplified genetic markers for reliable identification of Bacillus anthracis and its discrimination from other closely related bacterial species of the Bacillus cereus group. By combining polymerase chain reaction (PCR) amplification of six B. anthracis-specific genes (plasmid-associated genes encoding virulence factors (cyaA, **pagA**, lef, and capA, **capB**, capC) and one chromosomal marker BA-5449) with analysis of amplicons by microarray **hybridization**, we were able to unambiguously identify and discriminate B. anthracis among other closely related species. Bacillus identification relied on **hybridization** with multiple individual microarray **oligonucleotide probes** (oligoprobes) specific to each target B. anthracis gene. Evaluation of the assay was conducted using several B. anthracis strains (with or without pXO1 and pXO2 plasmids) as well as over 50 other species phylogenetically related to B. anthracis, including B. cereus, B. thuringiensis, B. mycoides, and B. subtilis. The developed microarray analysis of amplified genetic markers protocol provides an efficient method for (i) unambiguous identification and discrimination of B. anthracis from other Bacillus species and (ii) distinguishing between plasmid-containing and plasmid-free Bacillus anthracis strains.

L4 ANSWER 5 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-450920 [43] WPIDS
DOC. NO. CPI: C2003-119997
TITLE: Detecting Bacillus anthracis in a sample by

amplifying B.anthracis **capB**, **pagA** and lef nucleic acids followed by **hybridization** with labelled **capB**, **pagA** and lef **probes**, and detection by fluorescence resonance energy transfer.

DERWENT CLASS: B04 D16

INVENTOR(S): BELL, C A; COCKERILL, F R; UHL, J R; COCKERILL, F; UHL, J

PATENT ASSIGNEE(S): (MAYO-N) MAYO FOUND MEDICAL EDUCATION & RES; (HOFF) ROCHE DIAGNOSTICS GMBH; (BELL-I) BELL C A; (COCK-I) COCKERILL F; (UHLJ-I) UHL J

COUNTRY COUNT: 31

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1304387	A1	20030423	(200343)*	EN	31
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR					
US 2003082563	A1	20030501	(200343)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1304387	A1	EP 2002-22398	20021010
US 2003082563	A1 Provisional	US 2001-329826P	20011015
		US 2002-68238	20020205

PRIORITY APPLN. INFO: US 2002-68238 20020205; US 2001-329826P 20011015

AN 2003-450920 [43] WPIDS

AB EP 1304387 A UPAB: 20030707

NOVELTY - Detecting (M1) Bacillus anthracis (Ba) in a biological or non-biological sample, comprising:

(a) amplifying a portion of Ba **capB** and/or **pagA** and/or lef nucleic acids using specific primers;

(b) contacting the sample with a pair of **capB** and/or **pagA** and/or lef **probes** labelled with fluorescent moieties; and

(c) detecting the presence or absence of fluorescence resonance energy transfer between the **probes**, is new.

DETAILED DESCRIPTION - Detecting (M1) Bacillus anthracis (Ba) in a biological or non-biological sample, comprising:

(a) performing at least one cycling step which comprises an amplifying step and a **hybridizing** step, where the amplifying step comprises contacting the sample with:

(i) a pair of encapsulation protein B (**capB**) primers to produce a **capB** amplification product if a Ba **capB** nucleic molecule is present in the sample;

(ii) a pair of protective antigen (**pagA**) primers to produce **pagA** amplification product if a Ba **pagA** nucleic molecule is present in the sample; and/or

(iii) a pair of lethal factor (lef) primers to produce lef amplification product if a Ba lef nucleic molecule is present in the sample; and the **hybridization** step comprises contacting the sample with:

(iv) a pair of **capB probes**;

(v) a pair of **pagA probes**; and/or

(vi) a pair of lef **probes**, where the members of the pair of **probes hybridize** within no more than five nucleotides of each other, where a first **probe** of the pair **probes** is labelled with a donor fluorescent moiety and the second **probe** of the pair of **probes** is labelled with a corresponding acceptor fluorescent moiety; and

(b) detecting the presence or absence of fluorescence resonance energy transfer (FRET) between the donor fluorescent moiety of the first **probe** and the acceptor fluorescent moiety of the second **probe**, where the presence of FRET is indicative of the presence of Ba in the sample, and where the absence of FRET is indicative of the absence of Ba in the sample, is new.

INDEPENDENT CLAIMS are also included for the following:

(1) an article of manufacture, comprising a pair of **capB** primers, a pair of **capB probes**, and a donor fluorescent moiety and a corresponding acceptor fluorescent moiety;

(2) an article of manufacture comprising a pair of **pagA** primers, a pair of **pagA probes**, and a donor fluorescent moiety and a corresponding acceptor fluorescent moiety; and

(3) an article of manufacture, comprising a pair of lef primers, a pair of lef **probes**, and the donor fluorescent moiety and a corresponding acceptor fluorescent moiety.

USE - The method is useful for detecting the presence of Ba in a biological sample from an individual or in a non-biological sample (claimed). The method is useful for identifying Ba DNA from specimens for diagnosis of Ba infection and to identifying hoax cases of Ba. The methods can also used for Ba efficacy studies or epidemiology studies.

ADVANTAGE - The method is rapid, and allows real-time detection of Ba in a biological sample or in a non-biological sample. The method is more sensitive and specific then existing assays. The increased sensitivity or real-time PCR for detecting of Ba compared to other methods, as well as the improved features of real-time PCR including sample containment and real-time detection of the amplified product, make feasible the implementation of this technology for routine diagnosis of Ba infections in the clinical laboratory.

Dwg.0/0

L4 ANSWER 6 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-543517 [49] WPIDS
DOC. NO. NON-CPI: N2000-402041
DOC. NO. CPI: C2000-161758
TITLE: New polynucleotide encoding a functional binding partner of a Smad for treating diseases and disorders associated with aberrant levels of activity of a transforming growth factor-beta superfamily member.
DERWENT CLASS: B04 D16 P31
INVENTOR(S): WANG, T
PATENT ASSIGNEE(S): (GEHO) GEN HOSPITAL CORP; (WANG-I) WANG T
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000047102	A2	20000817	(200049)*	EN	200
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
US 2002076799	A1	20020620	(200244)		

US 6906179 B2 20050614 (200540)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000047102	A2	WO 2000-US3561	20000211
US 2002076799	A1 Provisional	US 1999-119786P	19990211
	CIP of	WO 2000-US3561	20000211
		US 2001-927738	20010810
US 6906179	B2 Provisional	US 1999-119786P	19990211
	CIP of	WO 2000-US3561	20000211
		US 2001-927738	20010810

PRIORITY APPLN. INFO: US 1999-119786P 19990211; US 2001-927738 20010810

AN 2000-543517 [49] WPIDS

AB WO 200047102 A UPAB: 20001006

NOVELTY - A purified polynucleotide (A) with a sequence of 989 (I), 1673 (II), 926 (III), 844 (IV), 216 (V), 261 (VI), or 547 (VII) nucleotides, given in the specification, that encodes a functional binding partner of a Smad, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) an expression vector comprising (A);

(2) a host cell transformed with (1);

(3) a polypeptide encoded by (1);

(4) a polypeptide with a sequence of 277 (VIII), 543 (IX), 396 (X), 255 (XI), 198 (XII), 414 (XIII), 294 (XIV), 329 (XV), 233 (XVI), 308 (XVII), 118 (XVIII), 72 (XIX), or 152 (XX) amino acids, given in the specification;

(5) an antibody to (3) or (4);

(6) a composition comprising Smad 1 and an interaction partner (IP) that is a beta subunit of the 20S proteasome (HsN3), antizyme, proliferation associated gene (**PAG**), glutathione-S-transferase (GST), tumor associated gene, atropin-1 interacting protein (AIP4), ribonuclear protein (U1SnRNP), a protein that interacts with the thyroid hormone receptor (TRIP4), Ran GTP binding protein 5, P0 acidic ribosomal phosphoprotein, beta -tubulin, KIAA 00104, (VIII), (IX), (X), (XII), (XV), (XVI), (XVII), or (XIX);

(7) a composition comprising Smad2 and an IP that is GST, AIP4, TRIP4, KIAA 00104, or (X);

(8) a composition comprising Smad3 and an IP that is HsN3, KIAA0104, human enhancer of filamentation (HEF1), prolyl-isomerase (FKBP25), AIP4, SnRNP C, a protein that interacts with the tumor suppressor protein retinoblastoma (RBP2), TRIP4, hnRNP A1, GST, (XV), (XVII), (XVI), (XXI), (XVIII), or (XX);

(9) identifying a compound which modulates the interaction of a protein with an IP comprising contacting the protein and IP in the presence of the compound and detecting the binding of the protein to the IP;

(10) identifying a candidate compound which modulates the interaction between a protein and an IP in yeast cells comprising:

(a) transforming yeast cells with expression constructs containing:

(i) a reporter gene linked to a DNA sequence bound by a second protein;

(ii) a gene comprising a first protein fused to a DNA binding

domain of the second protein; and

(iii) a gene comprising the IP and a transactivation domain;

(b) culturing the transformed cells of (a) in the presence of the compound; and

(c) detecting expression of the reporter gene;

(11) the method of (10), using a mammalian cell line instead of yeast cells;

(12) identifying a candidate compound which modulates the activity of an enzyme comprising expressing the enzyme from a recombinant expression construct and measuring the activity of the enzyme in the presence of the compound;

(13) monitoring the proteasome-mediated proteolysis of a protein comprising contacting an isolated polypeptide containing a protein of interest with isolated proteasomes and a mammalian cell extract in the presence and absence of a specific proteasome inhibitor and detecting the amount of the protein of interest;

(14) identifying a candidate compound which modulates the proteolysis of a protein comprising:

(a) transforming yeast cells with expression constructs containing:

(i) a hybrid protein comprising from the amino to carboxyl termini, a DNA binding domain, a protein of interest and a transactivation domain; and

(ii) a reporter gene comprising a DNA sequence bound by the DNA binding domain and transactivated by the transactivation domain;

(b) culturing the cells in the presence compound; and

(c) detecting the amount of reporter gene expression;

(15) monitoring the proteolysis of a protein of interest in mammalian cells comprising transfecting a mammalian cell line with the expression constructs of (14) and detecting the expression of the reporter gene;

(16) the method of (14), using a mammalian cell line instead of yeast cells;

(17) identifying novel, tissue-specific Smad interactors comprising:

(a) transforming yeast cells with expression constructs containing:

(i) a hybrid gene comprising the coding sequences for a full length Smad and DNA binding domain;

(ii) a cDNA library, derived from a single tissue or cell type, cloned into a vector which fuses the library sequences to a transactivation domain; and

(iii) a reporter gene, comprising a DNA sequence bound by the DNA binding domain, and transactivated by the transactivation domain;

(b) selecting yeast cell clones which express the reporter gene;

(c) probing DNA isolated from the clones with probes specific for all known Smad interactor proteins to identify clones which are novel; and

(d) using the sequences of clones identified in (c) as probes of multi-tissue Northern blots to confirm tissue-specific expression of the clones identified in (c);

(18) identifying novel Smad proteins comprising:

(1) steps (a) and (b) of (17);

(2) probing DNA isolated from the clones with nucleic acid probes derived from known Smads under conditions which permit the identification of yeast colonies which contain sequences that hybridize with known Smad sequences;

(3) isolating and sequencing the plasmid DNA sequences identified in (c); and

(4) comparing the resulting sequences with known Smad sequences, such that clones with sequences not identical to the sequence of known Smads are identified as novel;

(19) a composition comprising a ternary complex containing Smad1, HsN3 and antizyme;

(20) a composition comprising a quarternary complex comprising Smad1, Smad4, HsN3 and antizyme;

(21) a composition comprising one or more of antizyme and HsN3 or HEF1 and antizyme; and

(22) compositions comprising Smad1 nuclear interactor protein 1 (SNIP1) and the transcriptional co-activator CBP/p300.

ACTIVITY - Nephrotropic; cardiant; osteopathic; dermatological; immunosuppressive; vulnerary; vasotropic; cytostatic. No biological data is given.

MECHANISM OF ACTION - None given.

USE - The new polynucleotide is used in a expression vector to transform a host cell which can then express functional binding partners of Smads. Compounds are screened to identify those which can modulate the interaction of a protein with a known interaction partner. The proteasome-mediated proteolysis of a protein is monitored. Novel, tissue-specific Smad interactors and Smad proteins are identified (all claimed). Diseases and disorders associated with aberrant levels of activity of a transforming growth factor- beta superfamily member can be treated, such as kidney disease, cardiovascular diseases, osteoporosis, scleroderma, abnormalities of male fertility, neurodegenerative diseases, immunosuppression, wounds, hereditary hemorrhage telanangiectasia, cancer and eye diseases. Dwg.0/37

L4 ANSWER 7 OF 12 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2001:1814 BIOSIS
DOCUMENT NUMBER: PREV200100001814
TITLE: Identification and characterization of two Haemophilus influenzae type b capsule mutants.
AUTHOR(S): Schirmer, P. L. [Reprint author]; Satola, S. W. [Reprint author]; Turner, J. S. [Reprint author]; Whitney, C. G.; Yang, Y. H.; Farley, M. M. [Reprint author]
CORPORATE SOURCE: Atlanta VA Med. Ctr., Emory Univ., Atlanta, GA, USA
SOURCE: Abstracts of the Interscience Conference on Antimicrobial Agents and Chemotherapy, (2000) Vol. 40, pp. 44. print.
Meeting Info.: 40th Interscience Conference on Antimicrobial Agents and Chemotherapy. Toronto, Ontario, Canada. September 17-20, 2000. Interscience Conference on Antimicrobial Agents and Chemotherapy; American Society of Microbiology.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 21 Dec 2000
Last Updated on STN: 21 Dec 2000

L4 ANSWER 8 OF 12 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN

ACCESSION NUMBER: 1999-601132 [51] WPIDS
DOC. NO. NON-CPI: N1999-443162
DOC. NO. CPI: C1999-174950

TITLE: New bovine polypeptides useful for early diagnosis of pregnancy.
DERWENT CLASS: A96 B04 C06 D16 S03
INVENTOR(S): GREEN, J A; ROBERTS, R M; XIE, S
PATENT ASSIGNEE(S): (UMOR) UNIV MISSOURI; (GREE-I) GREEN J A; (ROBE-I) ROBERTS R M; (XIES-I) XIE S
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9947934	A2	19990923	(199951)*	EN	117
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9931028	A	19991011	(200008)		
EP 1141727	A2	20011010	(200167)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
MX 2000009241	A1	20010401	(200171)		
AU 768018	B	20031127	(200404)		
NZ 507033	A	20040625	(200445)		
US 6869770	B1	20050322	(200521)		
US 2005100975	A1	20050512	(200532)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9947934	A2		WO 1999-US6038	19990319
AU 9931028	A		AU 1999-31028	19990319
EP 1141727	A2		EP 1999-912715	19990319
			WO 1999-US6038	19990319
MX 2000009241	A1		MX 2000-9241	20000920
AU 768018	B		AU 1999-31028	19990319
NZ 507033	A		NZ 1999-507033	19990319
			WO 1999-US6038	19990319
US 6869770	B1	Provisional	US 1998-78783P	19980320
		Provisional	US 1998-106188P	19981028
			US 1999-273164	19990319
US 2005100975	A1	Provisional	US 1998-78783P	19980320
		Provisional	US 1998-106188P	19981028
		Cont of	US 1999-273164	19990319
			US 2003-655547	20030904

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9931028	A	Based on	WO 9947934
EP 1141727	A2	Based on	WO 9947934
AU 768018	B	Previous Publ.	AU 9931028
		Based on	WO 9947934
NZ 507033	A	Based on	WO 9947934
US 2005100975	A1	Cont of	US 6869770

PRIORITY APPLN. INFO: US 1998-106188P 19981028; US

Searcher : Shears 571-272-2528

1998-78783P 19980320; US
1999-273164 19990319; US
2003-655547 20030904

AN 1999-601132 [51] WPIDS
AB WO 9947934 A UPAB: 19991207
NOVELTY - A new method for early detection of pregnancy comprises using a pregnancy associated glycoprotein (**PAG**).

DETAILED DESCRIPTION - Pregnancy in a bovine (I) is detected by detecting at least one **PAG** which is present in early pregnancy and absent at about two months post-partum, and detecting pregnancy in a non-bovine Eurtherian (II) animal comprises detecting at least one **PAG** present in early pregnancy, where detection indicates the animal is pregnant.

INDEPENDENT CLAIMS are also included for the following:

(1) isolated BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 and BoPAG21 polypeptides;

(2) isolated BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 and BoPAG21 nucleic acids;

(3) an antibody composition (III) that reacts immunologically with BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 or BoPAG21, or individually with each antigen;

(4) a hybridoma cell (IV) that secretes a monoclonal antibody that reacts immunologically with BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 or BoPAG21, or individually with each antigen;

(5) preparation of a monoclonal antibody to BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoP AG17, BoPAG18, BoPAG19, BoPAG20 or BoPAG21, comprising immunizing an animal with a BoPAG preparation, obtaining antibody secreting cells from the animal, immortalizing the cells, and identifying a cell that secrets the appropriate antibodes;

(6) identifying a **PAG** that is an early indicator of pregnancy in a Eurtherian animal, comprising obtaining a cDNA library prepared from the placenta of the animal between days 15 and 30 of pregnancy, and **hybridizing** the library to a **PAG** -derived nucleic acid **probe**;

(7) identifying a **PAG** that is an early indicator of pregnancy in a Eurtherian animal, comprising obtaining an RNA preparation from the placenta of the animal between days 15 and 30 of pregnancy, and performing RT-PCR using **PAG**-derived primers;

(8) an **oligonucleotide** comprising at least 15 consecutive bases of BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 or BoPAG21, or their complements; and

(9) a kit comprising a first monoclonal antibody preparation that binds to BoPAG2, BoPAG4, BoPAG5, BoPAG6, BoPAG7, BoPAG9, BoPAG7v, BoPAG9v, BoPAG15, BoPAG16, BoPAG17, BoPAG18, BoPAG19, BoPAG20 or BoPAG21, and a suitable container.

USE - The new method is useful for detecting pregnancy in a bovine or a non-bovine Eurtherian animal, preferably of the suborder Ruminantia, family Bovidae, and is a goat or preferably a sheep; or order Perissodactyla, and is a rhinoceros or preferably a horse; or order carnivora, and is a cat, dog or human (claimed).

ADVANTAGE - Prior art methods for detecting pregnancy using BoPAG1 are unreliable, and BoPAG1 can only be detected at day 30 if artificially inseminated (new method can detect BoPAG at day 15), or

after 70 days post-partum.
Dwg.0/6

L4 ANSWER 9 OF 12 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 1998380520 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9712687
TITLE: Identification of PhoP-PhoQ activated genes within a duplicated region of the Salmonella typhimurium chromosome.
AUTHOR: Gunn J S; Belden W J; Miller S I
CORPORATE SOURCE: Department of Medicine, University of Washington, HSB K-140, Box 357710, Seattle, WA 98195, USA.
CONTRACT NUMBER: AI 30479 (NIAID)
SOURCE: Microbial pathogenesis, (1998 Aug) Vol. 25, No. 2, pp. 77-90.
Journal code: 8606191. ISSN: 0882-4010.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF013776
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19981008
Last Updated on STN: 20000303
Entered Medline: 19980929

AB Salmonellae virulence requires the PhoP-PhoQ two-component regulatory system. PhoP-PhoQ activate the transcription of genes following phagocytosis by macrophages which are necessary for survival within the phagosome environment. Thirteen previously undefined PhoP-activated gene fusions generated by MudJ and TnphoA (**pag A**, and E-P, respectively) were cloned and sequenced. Most pag products show no similarity to proteins in the database, while others are predicted to encode: a UDP-glucose dehydrogenase (**pagA**); a protein with similarity to the product of an E. coli aluminium-induced gene (pagH); a protein encoded within a Salmonella-unique region adjacent to the sinR gene (pagN); a protein similar to a product of the Yersinia virulence plasmid (pagO); and a protein with similarity to CrcA which is necessary for resistance of E. coli to camphor (pagP). Of the pag characterized, only pagK, M and O were closely linked. pagJ and pagK were shown to be unlinked but nearly identical in DNA sequence, as each was located within a 1.6 kb DNA duplication. The translations of sequences surrounding pagJ and pagK show similarity to proteins from extrachromosomal elements as well as those involved in DNA transposition and rearrangement, suggesting that this region may have been or is a mobile element. The transcriptional start sites of pagK, M, and J were determined; however, comparison to other known pag gene promoters failed to reveal a consensus sequence for PhoP-regulated activation. DNA sequences **hybridizing** to a Salmonella typhimurium pagK specific **probe** were found in S. enteritidis but absent in other Salmonella serotypes and Enterobacteriaceae tested, suggesting that these genes are specific for broad host range Salmonellae that cause diarrhoea in humans. Cumulatively, these data further demonstrate: (1) that PhoP-PhoQ is a global regulator of the production of diverse envelope or secreted proteins; (2) that PhoP-PhoQ regulate the production of proteins of redundant function; and (3) that pag are often located in regions of horizontally acquired DNA that are absent in other Enterobacteriaceae.

L4 ANSWER 10 OF 12 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN

ACCESSION NUMBER: 95244291 EMBASE
DOCUMENT NUMBER: 1995244291
TITLE: The elucidation of novel capsular genotypes of Haemophilus influenzae type b with the polymerase chain reaction.
AUTHOR: Leaves N.I.; Falla T.J.; Crook D.W.M.
CORPORATE SOURCE: Oxford Public Health Laboratory, John Radcliffe Infirmary,Headington, Oxford OX3 9DU, United Kingdom
SOURCE: Journal of Medical Microbiology, (1995) Vol. 43, No. 2, pp. 120-124. .
ISSN: 0022-2615 CODEN: JMMIAV
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 12 Sep 1995
Last Updated on STN: 12 Sep 1995

AB Molecular characterisation is an important pre-requisite for post-vaccine studies of Haemophilus influenzae type b (Hib). Three capsular genotyping patterns, b(S), b(G) and b(V), have been described in the major phylogenetic lineage of Hib. However, in a recent series of prospective studies, three new **hybridisation** patterns were observed among 425 strains of Hib. Four pairs of polymerase chain reaction (PCR) primers were used to identify the capsular gene (cap) structure of these Hib strains. This showed that the strains possessed simple DNA re-arrangements. In two instances a change in restriction enzyme recognition site was the most likely cause of the new **hybridisation** pattern. The third strain possessed a **cap b** locus consisting of intact tandem repeats of **cap b** in a b(S) background. It was reasoned that a similar **cap b** locus would not be readily recognised by **hybridisation** in a b(G) background, and b(G) strains were therefore characterised by the PCR method. This showed one of 35 b(G) strains to possess a cap locus with intact tandem repeat copies of **cap b**. The novel capsular genotypes described here are rare, but can be detected rapidly and accurately by a combination of PCR and capsular genotyping **hybridisation** patterns.

L4 ANSWER 11 OF 12 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 94288636 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8017940
TITLE: Identification of capsule-forming Bacillus anthracis spores with the PCR and a novel dual-**probe hybridization** format.
AUTHOR: Reif T C; Johns M; Pillai S D; Carl M
CORPORATE SOURCE: Accelerated Product Development Program, Naval Medical Research Institute, National Naval Medical Center, Bethesda, Maryland 20889.
SOURCE: Applied and environmental microbiology, (1994 May) Vol. 60, No. 5, pp. 1622-5.
Journal code: 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

Searcher : Shears 571-272-2528

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199407
ENTRY DATE: Entered STN: 19940810
Last Updated on STN: 19940810
Entered Medline: 19940728

AB Anthrax is a fatal infection of humans and livestock that is caused by the gram-positive bacterium Bacillus anthracis. The virulent strains of B. anthracis are encapsulated and toxigenic. In this paper we describe the development of a PCR technique for identifying spores of B. anthracis. Two 20-mer **oligonucleotide** primers specific for the **capB** region of 60-MDa plasmid pXO2 were used for amplification. The amplification products were detected by using biotin- and fluorescein-labeled **probes** in a novel dual-**probe hybridization** format. Using the combination of PCR amplification and dual-**probe hybridization**, we detected two copies of the bacterial genome. Because the PCR assay could detect a minimum of 100 unprocessed spores per PCR mixture, we attempted to facilitate the release of DNA by comparing the effect of limited spore germination with the effect of mechanical spore disruption prior to PCR amplification. The two methods were equally effective and allowed us to identify single spores of B. anthracis in PCR mixtures.

L4 ANSWER 12 OF 12 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 94322370 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8046736
TITLE: Analysis by pulsed-field gel electrophoresis of insertion mutations in the transferrin-binding system of Haemophilus influenzae type b.
AUTHOR: Curran R; Hardie K R; Towner K J
CORPORATE SOURCE: Department of Microbiology, University Hospital, Queen's Medical Centre, Nottingham.
SOURCE: Journal of medical microbiology, (1994 Aug) Vol. 41, No. 2, pp. 120-6.
Journal code: 0224131. ISSN: 0022-2615.
PUB. COUNTRY: SCOTLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19940909
Last Updated on STN: 20021218
Entered Medline: 19940901

AB A mutagenesis system involving the insertion of a non-transposable antibiotic resistance gene cassette was used to generate stable mutations in the chromosome of Haemophilus influenzae type b strain Eagan. The mutations generated were shown by pulsed-field gel electrophoresis (PFGE) to have unique SmaI fingerprint patterns and to be located randomly on the chromosome. Of 700 insertion mutants screened, 29 had stable insertions resulting in constitutive expression of transferrin-binding proteins (TBPs). The high proportion of such mutants indicated that numerous regulatory loci could influence the expression of this phenotype. Five such regulatory mutations were analysed in detail by PFGE and DNA **hybridisation** and were shown to be located at five different chromosomal loci, although three of the five loci were located on the same 330-kb SmaI fragment of the wild-type strain Eagan chromosome. This fragment also contains several important virulence determinants, including the **capb** locus, and one of the five constitutive

mutants had concomitantly lost the ability to synthesise a type-b capsule. No DNA homology was demonstrated between H. influenzae chromosomal fragments separated by PFGE and DNA **probes** for the TBPs from Neisseria meningitidis, but the possibility of shared regulatory mechanisms controlling the expression of TBPs in these two species remains to be investigated.

FILE 'USPATFULL' ENTERED AT 17:12:21 ON 19 APR 2006
CA INDEXING COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 18 Apr 2006 (20060418/PD)
FILE LAST UPDATED: 18 Apr 2006 (20060418/ED)
HIGHEST GRANTED PATENT NUMBER: US7032245
HIGHEST APPLICATION PUBLICATION NUMBER: US2006080750
CA INDEXING IS CURRENT THROUGH 18 Apr 2006 (20060418/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 18 Apr 2006 (20060418/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Feb 2006
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Feb 2006

L5 65318 SEA FILE=USPATFULL ABB=ON PLU=ON (OLIGONUCLEOTIDE OR OLIGO NUCLEOTIDE OR PROBE)(S)(HYBRIDIS? OR HYBRIDIZ?)
L6 10 SEA FILE=USPATFULL ABB=ON PLU=ON L5(S)(PAGA OR "PAG A" OR CAPB OR "CAP B")

L6 ANSWER 1 OF 10 USPATFULL on STN

ACCESSION NUMBER:	2004:273669 USPATFULL
TITLE:	Methods and systems for producing recombinant viral antigens
INVENTOR(S):	Zebedee, Suzanne, Carlsbad, CA, UNITED STATES Inchauspe, Genevieve, Lyon, FRANCE Nasoff, Marc S., San Diego, CA, UNITED STATES Prince, Alfred M., Pound Ridge, NY, UNITED STATES Helting, Torsten B., San Francisco, CA, UNITED STATES Nunn, Michael F., Washington, DC, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004214163	A1	20041028
APPLICATION INFO.:	US 2003-677956	A1	20031001 (10)

RELATED APPLN. INFO.:	Division of Ser. No. US 1997-931855, filed on 16 Sep 1997, GRANTED, Pat. No. US 6692751 Continuation-in-part of Ser. No. US 1995-563733, filed on 28 Nov 1995, ABANDONED Division of Ser. No. US 1993-49531, filed on 20 Apr 1993, GRANTED, Pat. No. US 5470720 Division of Ser. No. US 1989-344237, filed on 26 Apr 1989, GRANTED, Pat. No. US 5204259 Continuation-in-part of Ser. No. US 1988-191229, filed on 6 May 1988, ABANDONED
DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	Joseph E. Mueth, Esq., Joseph E. Mueth Law Corporation, 8th Floor, 225 South Lake Avenue, Pasadena, CA, 91101
NUMBER OF CLAIMS:	75
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	9 Drawing Page(s)
LINE COUNT:	2448

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to recombinant expression vectors which express segments of deoxyribonucleic acid that encode recombinant HIV and HCV antigens. These recombinant expression vectors are transformed into host cells and used in a method to express large quantities of these antigens. The invention also provides compositions containing certain of the isolated antigens, diagnostic systems containing these antigens and methods of assaying body fluids to detect the presence of antibodies against the antigens of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 2 OF 10 USPATFULL on STN

ACCESSION NUMBER:	2004:41347 USPATFULL
TITLE:	Methods and systems for producing recombinant viral antigens
INVENTOR(S):	Zebedee, Suzanne, Carlsbad, CA, United States Inchauspe, Genevieve, Lyons, FRANCE Nasoff, Marc S., San Diego, CA, United States Prince, Alfred S., Pound Ridge, NY, United States Helting, Torsten B., P.O. Box 880963, San Francisco, CA, United States 94188 Nunn, Michael F., Washington, DC, United States
PATENT ASSIGNEE(S):	New York Blood Center, New York, NY, United States (U.S. corporation) by said Genevieve Inchauspe and Alfred Prince Helting, Torsten B., San Francisco, CA, United States (U.S. individual)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6692751	B1	20040217
APPLICATION INFO.:	US 1997-931855		19970916 (8)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1995-563733, filed on 28 Nov 1995, now abandoned Division of Ser. No. US 1993-49531, filed on 20 Apr 1993, now patented, Pat. No. US 5470720 Division of Ser. No. US 1989-344237, filed on 26 Apr 1989, now patented, Pat. No. US 5204259 Continuation-in-part of Ser. No. US 1988-258016, filed on 14 Oct 1988, now abandoned Continuation-in-part of Ser. No. US 1988-206499, filed on 13 Jun 1988, now abandoned Continuation-in-part of Ser. No. US 1988-191229, filed on 6 May 1988, now abandoned Continuation-in-part of Ser. No. US 931855 Continuation-in-part of Ser. No. US 1994-272271, filed on 8 Jul 1994, now abandoned Continuation of Ser. No. US 1990-616369, filed on 21 Nov 1990, now abandoned Continuation-in-part of Ser. No. US 1990-573643, filed on 27 Aug 1990, now abandoned

DOCUMENT TYPE:	Utility
FILE SEGMENT:	GRANTED
PRIMARY EXAMINER:	Scheiner, Laurie
ASSISTANT EXAMINER:	Parkin, J. S.
LEGAL REPRESENTATIVE:	Mueth, Joseph E.
NUMBER OF CLAIMS:	14
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	9 Drawing Figure(s); 9 Drawing Page(s)
LINE COUNT:	2181

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to recombinant expression vectors which express segments of deoxyribonucleic acid that encode recombinant HIV and HCV antigens. These recombinant expression vectors are transformed into host cells and used in a method to express large quantities of these antigens. The invention also provides compositions containing certain of the isolated antigens., diagnostic systems containing these antigens and methods of assaying body fluids to detect the presence of antibodies against the antigens of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 3 OF 10 USPATFULL on STN

ACCESSION NUMBER: 2003:288604 USPATFULL

TITLE: Species specific identification of spore-producing microbes using the gene sequence of small acid-soluble spore coat proteins for amplification based diagnostics

INVENTOR(S): Hunter-Cevera, Jennifer C., Ellicott City, MD, UNITED STATES
Leighton, Terrance, Lafayette, CA, UNITED STATES
Goldman, Stan, Walnut Creek, CA, UNITED STATES
Longchamp, Pascal, Palo Alto, CA, UNITED STATES
McKinney, Nancy, La Honda, CA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003203362	A1	20031030
APPLICATION INFO.:	US 2002-67613	A1	20020204 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-590759, filed on 8 Jun 2000, GRANTED, Pat. No. US 6472155

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-192206P	20000327 (60)
	US 1999-138167P	19990608 (60)

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834

NUMBER OF CLAIMS: 18

EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 7 Drawing Page(s)

LINE COUNT: 1095

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to methods and compositions for the detection of Bacillus species such as Bacillus anthracis and Bacillus globigii as well as Clostridium perfringens. It relies on nucleic acid sequence differences in spore protein genes carried in the genomic sequence of these organisms.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 4 OF 10 USPATFULL on STN

ACCESSION NUMBER: 2003:237907 USPATFULL

TITLE: Compositions and methods for the therapy and diagnosis of colon cancer

INVENTOR(S): King, Gordon E., Shoreline, WA, UNITED STATES
Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
Xu, Jiangchun, Bellevue, WA, UNITED STATES
Secrist, Heather, Seattle, WA, UNITED STATES
Jiang, Yuqiu, Kent, WA, UNITED STATES
PATENT ASSIGNEE(S): Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003166064	A1	20030904
APPLICATION INFO.:	US 2002-99926	A1	20020314 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2001-33528, filed on 26 Dec 2001, PENDING Continuation-in-part of Ser. No. US 2001-920300, filed on 31 Jul 2001, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-302051P	20010629 (60)
	US 2001-279763P	20010328 (60)
	US 2000-223283P	20000803 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
LINE COUNT: 8531
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 5 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:120082 USPATFULL
TITLE: Detection of bacillus anthracis
INVENTOR(S): Bell, Constance A., Mililani, HI, UNITED STATES
Uhl, James, Rochester, MN, UNITED STATES
Cockerill, Franklin, Rochester, MN, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003082563	A1	20030501
APPLICATION INFO.:	US 2002-68238	A1	20020205 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-329826P	20011015 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: FISH & RICHARDSON P.C., 3300 DAIN RASCHER PLAZA, 60

SOUTH SIXTH STREET, MINNEAPOLIS, MN, 55402
NUMBER OF CLAIMS: 56
EXEMPLARY CLAIM: 1
LINE COUNT: 1653
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides methods to detect B. anthracis in biological or non-biological samples using real-time PCR. Primers and probes for the detection of B. anthracis are provided by the invention. Articles of manufacture containing such primers and probes for detecting B. anthracis are further provided by the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 6 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2003:106233 USPATFULL
TITLE: Compositions and methods for the therapy and diagnosis of pancreatic cancer
INVENTOR(S): Benson, Darin R., Seattle, WA, UNITED STATES
Kalos, Michael D., Seattle, WA, UNITED STATES
Lodes, Michael J., Seattle, WA, UNITED STATES
Persing, David H., Redmond, WA, UNITED STATES
Hepler, William T., Seattle, WA, UNITED STATES
Jiang, Yuqiu, Kent, WA, UNITED STATES
PATENT ASSIGNEE(S): Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003073144	A1	20030417	
APPLICATION INFO.:	US 2002-60036	A1	20020130	(10)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-333626P	20011127	(60)
	US 2001-305484P	20010712	(60)
	US 2001-265305P	20010130	(60)
	US 2001-267568P	20010209	(60)
	US 2001-313999P	20010820	(60)
	US 2001-291631P	20010516	(60)
	US 2001-287112P	20010428	(60)
	US 2001-278651P	20010321	(60)
	US 2001-265682P	20010131	(60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
LINE COUNT: 14253
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly pancreatic cancer, are disclosed. Illustrative compositions comprise one or more pancreatic tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly pancreatic cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 7 OF 10 USPATFULL on STN

ACCESSION NUMBER:	2002:243051 USPATFULL
TITLE:	Compositions and methods for the therapy and diagnosis of ovarian cancer
INVENTOR(S):	Algate, Paul A., Issaquah, WA, UNITED STATES Jones, Robert, Seattle, WA, UNITED STATES Harlocker, Susan L., Seattle, WA, UNITED STATES
PATENT ASSIGNEE(S):	Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002132237	A1	20020919
APPLICATION INFO.:	US 2001-867701	A1	20010529 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-207484P	20000526 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
NUMBER OF CLAIMS:	11
EXEMPLARY CLAIM:	1
LINE COUNT:	25718

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly ovarian cancer, are disclosed. Illustrative compositions comprise one or more ovarian tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly ovarian cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 8 OF 10 USPATFULL on STN

ACCESSION NUMBER:	2002:242791 USPATFULL
TITLE:	Compositions and methods for the therapy and diagnosis of colon cancer
INVENTOR(S):	King, Gordon E., Shoreline, WA, UNITED STATES Meagher, Madeleine Joy, Seattle, WA, UNITED STATES Xu, Jiangchun, Bellevue, WA, UNITED STATES Secrist, Heather, Seattle, WA, UNITED STATES
PATENT ASSIGNEE(S):	Corixa Corporation, Seattle, WA, UNITED STATES (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002131971	A1	20020919
APPLICATION INFO.:	US 2001-33528	A1	20011226 (10)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 2001-920300, filed on 31 Jul 2001, PENDING		

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-302051P	20010629 (60)
	US 2001-279763P	20010328 (60)
	US 2000-223283P	20000803 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
LINE COUNT: 8083
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 9 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2001:220693 USPATFULL
TITLE: Recombinant vaccine for diseases caused by encapsulated organisms
INVENTOR(S): Inzana, Thomas J., Blacksburg, VA, United States
Ward, Christine, Irving, TX, United States
PATENT ASSIGNEE(S): Virginia Tech Intellectual Properties, Inc., Blacksburg, VA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6326001	B1	20011204
APPLICATION INFO.:	US 1998-115824		19980715 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1996-673814, filed on 27 Jun 1996
DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Saoud, Christine J.
ASSISTANT EXAMINER: Turner, Sharon
LEGAL REPRESENTATIVE: McGuireWoods LLP
NUMBER OF CLAIMS: 5
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 905
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Vaccines for diseases caused by normally encapsulated organisms are produced by genetically modifying those organisms by deleting the genes encoding for capsule synthesis or a portion thereof sufficient to produce non-capsulated mutants of the organisms. As an example, a live, attenuated strain of Actinobacillus pleuropneumoniae genetically modified with a large deletion in a chromosomal regions of the DNA which encodes for capsule synthesis is a safe and effective vaccine against swine pleuropneumonia.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 10 OF 10 USPATFULL on STN
ACCESSION NUMBER: 2000:87725 USPATFULL
TITLE: Recombinant vaccine for diseases caused by encapsulated organisms
INVENTOR(S): Inzana, Thomas J., Blacksburg, VA, United States
Ward, Christine, Irving, TX, United States
PATENT ASSIGNEE(S): Virginia Tech Intellectual Properties, Inc., Blacksburg, VA, United States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6086894		20000711	
APPLICATION INFO.:	US 1996-673814		19960627	(8)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Caputa, Anthony C.
ASSISTANT EXAMINER: Masood, Khalid
LEGAL REPRESENTATIVE: Whitham, Curtis, & Whitham
NUMBER OF CLAIMS: 4
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 13 Drawing Figure(s); 10 Drawing Page(s)
LINE COUNT: 1414
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Vaccines for diseases caused by normally encapsulated organisms are produced by genetically modifying those organisms by deleting the genes encoding for capsule synthesis or a portion thereof sufficient to produce non-capsulated mutants of the organisms. As an example, a live, attenuated strain of Actinobacillus pleuropneumoniae genetically modified with a large deletion in a chromosomal regions of the DNA which encodes for capsule synthesis is a safe and effective vaccine against swine pleuropneumonia.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

(FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 17:15:22 ON 19 APR 2006)

- Author(s)

L7 1002 S "NORMAN S"?/AU
L8 6 S "BUNGO J"?/AU
L9 3648 S "HOGAN J"?/AU
L10 203 S "WEISBURG W"?/AU
L11 2 S L7 AND L8 AND L9 AND L10
L12 3 S L7 AND (L8 OR L9 OR L10)
L13 6 S L8 AND (L9 OR L10)
L14 3 S L9 AND L10
L15 2 S (L7 OR L8 OR L9 OR L10) AND (PAGA OR "PAG A" OR CAPB OR "CAP B")
L16 7 S L11 OR L12 OR L13 OR L14 OR L15
L17 5 DUP REM L16 (2 DUPLICATES REMOVED)
L17 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2004:681670 CAPLUS
DOCUMENT NUMBER: 141:201314
TITLE: Assay and compositions for detection of Bacillus anthracis nucleic acid
INVENTOR(S): **Norman, Sylvia A.; Bungo, Jennifer J.; Hogan, James J.; Weisburg, William G.**
PATENT ASSIGNEE(S): Gen-Probe Incorporated, USA

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004070001	A2	20040819	WO 2003-US36240	20031112
WO 2004070001	A3	20051201		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2506151	AA	20040819	CA 2003-2506151	20031112
EP 1572977	A2	20050914	EP 2003-815297	20031112
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				

PRIORITY APPLN. INFO.:

US 2002-426552P	P	20021115
US 2003-471082P	P	20030516
WO 2003-US36240	W	20031112

AB The invention includes nucleic acid sequences and methods of detection of Bacillus anthracis that use oligonucleotide probes specific for genetic material contained in the pXO1 and pX02 plasmids in nucleic acid hybridization reactions. Embodiments of the method may include addnl. probes specific for other gene sequences to distinguish B. anthracis from other bacterial species present in a sample or to provide an indication that the assay was performed properly even when no Bacillus sequence is detected. The invention include oligonucleotides that hybridize to **capB** and **pagA** gene sequence.

L17 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2004:1019658 CAPLUS
DOCUMENT NUMBER: 142:751
TITLE: Compositions, methods and kits for determining the presence of Trichomonas vaginalis in a test sample
INVENTOR(S): **Weisburg, William G.; Bungo, Jennifer J.**
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 52 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

US 2004235138	A1	20041125	US 2004-848922	20040518
AU 2004276722	A1	20050407	AU 2004-276722	20040518
CA 2525413	AA	20050407	CA 2004-2525413	20040518
WO 2005031005	A2	20050407	WO 2004-US15742	20040518
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
EP 1633893	A2	20060315	EP 2004-809385	20040518
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
PRIORITY APPLN. INFO.:			US 2003-472028P	P 20030519
			WO 2004-US15742	W 20040518

AB The present invention relates to oligonucleotides useful for determining the presence of Trichomonas vaginalis in a test sample. The oligonucleotides of the present invention may be incorporated into detection probes, helper probes, capture probes and amplification oligonucleotides, and used in various combinations thereof.

L17 ANSWER 3 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:529081 BIOSIS
DOCUMENT NUMBER: PREV200300533357
TITLE: Rapid detection of Trichomonas vaginalis from vaginal specimens by transcription-mediated amplification.
AUTHOR(S): Sitay, A. [Reprint Author]; **Bungo**, J. [Reprint Author]; Dickey, K. [Reprint Author]; **Weisburg**, W. [Reprint Author]; Aguirre, T.; Fuller, D.; Jasper, L.; Davis, T.
CORPORATE SOURCE: Gen-Probe Incorporated, San Diego, CA, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. C-120. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003

AB Background: Trichomonas vaginalis (Tvag) is a common cause of sexually transmitted disease (STD), with an estimated 5 million new cases occurring annually in the U.S. Ten to 50% of infections are asymptomatic. Diagnosis of Tvag infection is problematic. The

commonly used wet mount, while rapid, has low sensitivity. Culture and Pap stain are lengthy procedures and technically challenging. A rapid, amplified assay system is described here for detection of Tvag. Methods: The test includes target capture, Transcription-Mediated Amplification (TMA) and a Hybridization Protection Assay (HPA). Target capture uses specific DNA capture oligos and magnetic beads for separation of target rRNA from clinical specimens. TMA amplifies a specific region of the target rRNA. HPA uses a chemiluminescent probe in a homogenous assay format whereby probe binds specifically to Tvag amplicon and is induced to emit light. Results: A total of 152 vaginal swabs from patients attending STD clinics were tested in the Tvag assay system at Gen-Probe Incorporated and compared with wet mount, In Pouch culture, BD Affirm, and Papstain performed at Wishard Memorial Hospital. Thirtysix specimens were positive by any one of the 4 comparator methods; 34 of these werepositive by TMA. One hundred sixteen specimens were negative for T. vaginalis by all 4 comparator methods; 95 of these were negative by TMA and 21 were positive by TMA. The apparent sensitivity and specificity of the TMA assay were 94% and 82%, respectively. It is unclear if the TMA+, comparator- specimens are TMA false positive results or reflect the greater sensitivity of target amplification. Fifteen of the 21 TMA+, comparator- specimens were positive on repeat TMA testing, suggesting that they may be true positives. If this is the case, the sensitivity and specificity would be 97% and 94%, respectively. The remaining six may be false positives or contain such low concentrations of T. vaginalis as tobe subject to sampling variation. Conclusions: Our results suggest that target amplification may be a more rapid and sensitive method to detect T. vaginalis than alternative methods, including culture.

L17 ANSWER 4 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2003:543078 BIOSIS
DOCUMENT NUMBER: PREV200300545967
TITLE: Development of a rapid culture identification test for Bacillus anthracis.
AUTHOR(S): Dickey, K. [Reprint Author]; **Norman, S. A.** [Reprint Author]; **Bungo, J.** [Reprint Author]; Sitay, A. [Reprint Author]; Marlowe, E. M. [Reprint Author]; Gordon, P. C. [Reprint Author]; **Weisburg, W.** [Reprint Author]; Moore, D.; Ferrero, D. V.
CORPORATE SOURCE: Gen-Probe Incorporated, San Diego, CA, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2003) Vol. 103, pp. C-169. http://www.asmusa.org/mtgsrc/generalmeeting.htm. cd-rom.
Meeting Info.: 103rd American Society for Microbiology General Meeting. Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
ISSN: 1060-2011 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 19 Nov 2003
Last Updated on STN: 19 Nov 2003

AB Background: Bacillus anthracis is an important pathogen and potential bioterrorism agent. While culture of the organism is relatively rapid and easy, definitive identification of a bacterial colony as B. anthracis is problematic for most microbiology laboratories.

Gen-Probe has developed a rapid assay system for the detection and identification of B. anthracis from culture. Methods: The test includes an organism lysis step and detection via Gen-Probe's Hybridization Protection Assay (HPA). It offers a convenient homogenous format in which chemiluminescent probes bind specifically to DNA virulence determinants of B. anthracis. A total of 177 cultures were tested at Gen-Probe Incorporated and at the Centers for Disease Control. Standard methods for identification, such as the gamma phage test, were used previously to identify 26 different stains as B. anthracis. Other strains tested included 126 strains from 20 different closely-related species of Bacillus (non-B. anthracis), strains from the genera Paenibacillus and Brevibacillus, and other potential agents of bioterrorism such as Yersinia pestis and Francisella tularensis. Many of the closely-related Bacillus spp. cultures tested at Gen-Probe were strains previously sent to two Public Health Laboratories in California as possible B. anthracis. Results: The analytical sensitivity of the test was 107 to 109 CFU/ml (approximately one small colony) for the detection of B. anthracis. All 26 strains of B. anthracis were positive with the test. None of the other cultures tested gave positive results with the test. Time to result was approximately one hour. Conclusions: Our results suggest that this culture identification test is a rapid, sensitive and specific method for the detection and identification of B. anthracis.

L17 ANSWER 5 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2002:189031 BIOSIS
DOCUMENT NUMBER: PREV200200189031
TITLE: A new method for the detection and identification of agents of bacteremia and fungemia.
AUTHOR(S): Bruckner, D. [Reprint author]; Gibson, L. [Reprint author]; Hindler, J. [Reprint author]; **Hogan**, J.; Andruszkiewicz, I.; Clark-Dickey, K.; **Weisburg**, W.
CORPORATE SOURCE: UCLA Medical Center, Los Angeles, CA, USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2001) Vol. 101, pp. 147. print.
Meeting Info.: 101st General Meeting of the American Society for Microbiology. Orlando, FL, USA. May 20-24, 2001. American Society for Microbiology.
ISSN: 1060-2011.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 13 Mar 2002
Last Updated on STN: 13 Mar 2002

AB Timely detection and identification of the causative agent of bacteremia and fungemia is of great clinical importance. The objectives of this study were: 1) to investigate a new screening method for early detection of positive blood cultures (BC) compared to the BacT/Alert (Organon Teknika) instrument (BTA); and 2) to investigate the results of a novel probe-matrix identification (ID) system to identify the causative agent(s) when either the new method or the BTA instrument signaled positive. The prototype screening test used an "all bacterial/all fungal" DNA probe mixture to detect rRNA from BC using the Gen-Probe Incorporated Hybridization Protection Assay (HPA). The prototype ID test used a novel DNA probe matrix

system of various bacterial and fungal "groups", genus or species probes used in combination to identify the microorganism from a positive BC. We tested 467 BC bottles by the new method and compared the results to routine culture and ID methods used at UCLA Medical Center. Each bottle was sampled daily, at 3 time points over the first 74 hours, or when the BTA signaled positive. Aliquots (0.4 mL) of each BC were washed in a buffered saponin solution, lysed by a heat method, and assayed by HPA in an automated microtiter plate format. Thirty-one of the 467 BC bottles were positive by the BTA. The organisms isolated included yeast (15), staphylococci (10), Enterococcus sp. (4), Streptococcus sp. (2), Enterobacter cloacae (1), Micrococcus sp. (1) and Listeria monocytogenes (1); mixed cultures were found in 4 BC. Of the positives, 12 of 31 were detected by the HPA method as much as 16.5 hours earlier than the BTA. Once the BTA signaled positive, all BC were simultaneously positive by the HPA method. Further testing of the BTA positive bottles using the probe-matrix ID system resulted in accurate organism identification. These new methods show promise to significantly shorten the time to detection and identification of the causative agent of bacteremia or fungemia.

FILE 'HOME' ENTERED AT 17:17:43 ON 19 APR 2006

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=> d his ful

     (FILE 'CAPLUS' ENTERED AT 17:09:49 ON 19 APR 2006)
                DEL HIS Y
L1         63345 SEA ABB=ON  PLU=ON  (OLIGONUCLEOTIDE OR OLIGO NUCLEOTIDE
                OR PROBE) AND (HYBRIDIS? OR HYBRIDIZ?)
L2             9 SEA ABB=ON  PLU=ON  L1 AND (PAGA OR PAG A OR CAPB OR CAP
                B)

     FILE 'CAPLUS' ENTERED AT 17:11:39 ON 19 APR 2006
                D QUE
                D 1-9 .BEVERLY

     FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO' ENTERED AT 17:11:40 ON 19 APR 2006
L3            24 SEA ABB=ON  PLU=ON  L2
L4            12 DUP REM L3 (12 DUPLICATES REMOVED)
                D 1-12 IBIB ABS

     FILE 'USPATFULL' ENTERED AT 17:12:21 ON 19 APR 2006
L*** DEL   73493 S (OLIGONUCLEOTIDE OR OLIGO NUCLEOTIDE OR PROBE)(L)(HYBRIDI
L*** DEL     271 S L5(S)(PAGA OR "PAG A" OR CAPB OR "CAP B")
L5         65318 SEA ABB=ON  PLU=ON  (OLIGONUCLEOTIDE OR OLIGO NUCLEOTIDE
                OR PROBE)(S)(HYBRIDIS? OR HYBRIDIZ?)
L6            10 SEA ABB=ON  PLU=ON  L5(S)(PAGA OR "PAG A" OR CAPB OR "CAP
                B")
                D QUE
                D 1-10 IBIB ABS

     FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO' ENTERED AT 17:15:22 ON 19 APR 2006
L7          1002 SEA ABB=ON  PLU=ON  "NORMAN S"?/AU
L8             6 SEA ABB=ON  PLU=ON  "BUNGO J"?/AU
L9          3648 SEA ABB=ON  PLU=ON  "HOGAN J"?/AU
L10          203 SEA ABB=ON  PLU=ON  "WEISBURG W"?/AU
L11            2 SEA ABB=ON  PLU=ON  L7 AND L8 AND L9 AND L10
L12            3 SEA ABB=ON  PLU=ON  L7 AND (L8 OR L9 OR L10)
L13            6 SEA ABB=ON  PLU=ON  L8 AND (L9 OR L10)
L14            3 SEA ABB=ON  PLU=ON  L9 AND L10
L15            2 SEA ABB=ON  PLU=ON  (L7 OR L8 OR L9 OR L10) AND (PAGA OR
                "PAG A" OR CAPB OR "CAP B")
L16            7 SEA ABB=ON  PLU=ON  L11 OR L12 OR L13 OR L14 OR L15
L17            5 DUP REM L16 (2 DUPLICATES REMOVED)
                D 1-5 IBIB ABS

     FILE 'HOME' ENTERED AT 17:17:43 ON 19 APR 2006


     FILE CAPLUS

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FILE COVERS 1907 - 19 Apr 2006 VOL 144 ISS 17
FILE LAST UPDATED: 18 Apr 2006 (20060418/ED)

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FILE MEDLINE
FILE LAST UPDATED: 18 APR 2006 (20060418/UP). FILE COVERS 1950 TO DA

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The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).
See also:

http://www.nlm.nih.gov/mesh/
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.ht
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE BIOSIS
FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 12 April 2006 (20060412/ED)

FILE EMBASE
FILE COVERS 1974 TO 19 Apr 2006 (20060419/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

EMBASE is now updated daily. SDI frequency remains weekly (default) and biweekly.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE WPIDS
FILE LAST UPDATED: 13 APR 2006 <20060413/UP>
MOST RECENT DERWENT UPDATE: 200625 <200625/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE, PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf

Searcher : Shears 571-272-2528

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>>> PLEASE BE AWARE OF THE NEW IPC REFORM IN 2006, SEE
http://www.stn-international.de/stndatabases/details/ipc_reform.html a
http://scientific.thomson.com/media/scpdf/ipcrdwpi.pdf <<<

>>> UPCOMING NEW DWPI: EFFECTS ON SCRIPT RUNS - SEE NEWS MESSAGE <<<

FILE CONFSCI
FILE COVERS 1973 TO 10 Apr 2006 (20060410/ED)

CSA has suspended updates until further notice.

FILE SCISEARCH

FILE COVERS 1974 TO 13 Apr 2006 (20060413/ED)

SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE JICST-EPLUS
FILE COVERS 1985 TO 17 APR 2006 (20060417/ED)

THE JICST-EPLUS FILE HAS BEEN RELOADED TO REFLECT THE 1999 CONTROLLED
TERM (/CT) THESAURUS RELOAD.

FILE JAPIO
FILE LAST UPDATED: 3 APR 2006 <20060403/UP>
FILE COVERS APRIL 1973 TO DECEMBER 22, 2005

>>> GRAPHIC IMAGES AVAILABLE <<<

>>> NEW IPC8 DATA AND FUNCTIONALITY NOT YET AVAILABLE IN THIS FILE.
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DEVELOPMENTS AND SEE OUR NEWS SECTION FOR FURTHER INFORMATION
ABOUT THE IPC REFORM <<<

FILE USPATFULL
FILE COVERS 1971 TO PATENT PUBLICATION DATE: 18 Apr 2006 (20060418/PD)
FILE LAST UPDATED: 18 Apr 2006 (20060418/ED)
HIGHEST GRANTED PATENT NUMBER: US7032245
HIGHEST APPLICATION PUBLICATION NUMBER: US2006080750
CA INDEXING IS CURRENT THROUGH 18 Apr 2006 (20060418/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 18 Apr 2006 (20060418/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Feb 2006
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Feb 2006

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